

Risk assessment for the deployment of a Costa Rican transgenic rice variety under tropical conditions

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COSTA RICA**

Costa Rica

Extension: **51,000 Km²**

Population: **4 millions**

Economy based on: **ecoturism, agriculture and high technology industry.**

38% of the territory is protected in governmental and private conservation areas.

5% of world biodiversity, including more than **11.000 plant species**

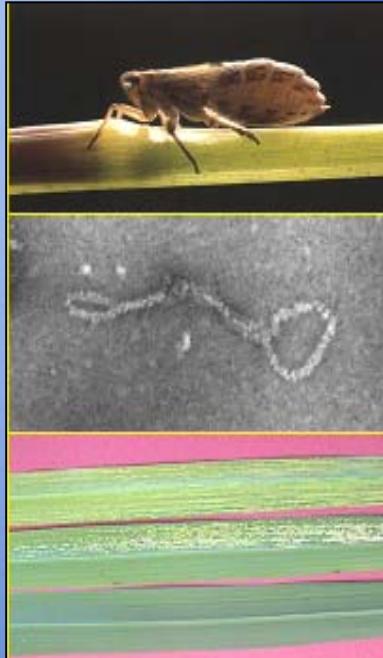
National Biosafety Committee since 1990.

National policies are:

Sustainable use of biodiversity and biotechnology.



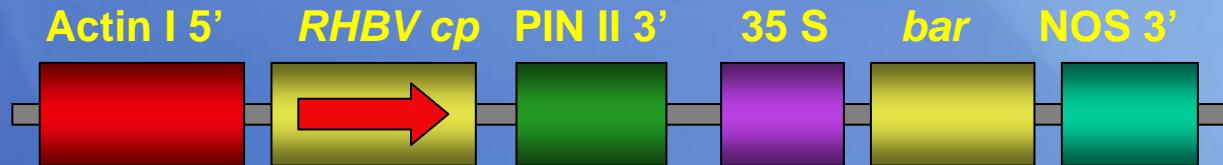
Genetic engineering of a Costa Rican *indica* rice variety by biolistics



Sequences of
rice hoja blanca
virus (RHBV)
nucleoprotein



Bar gene to confer
resistance to herbicide
PPT



Field evaluation of transgenic lines

Four field trials

- Morphological evaluation of lines
- Resistance to the herbicide PPT and to RHBV
- Selection of lines with best agronomic traits

Confined conditions

- Field trials in non rice growing areas
- Covered with bird-proof net
- Vegetative barriers surrounding field plot
- Destruction of remanents
- NBC supervision



Main objective

To study gene flow from *Oryza sativa* transgenic lines to related wild rice species and weedy rice



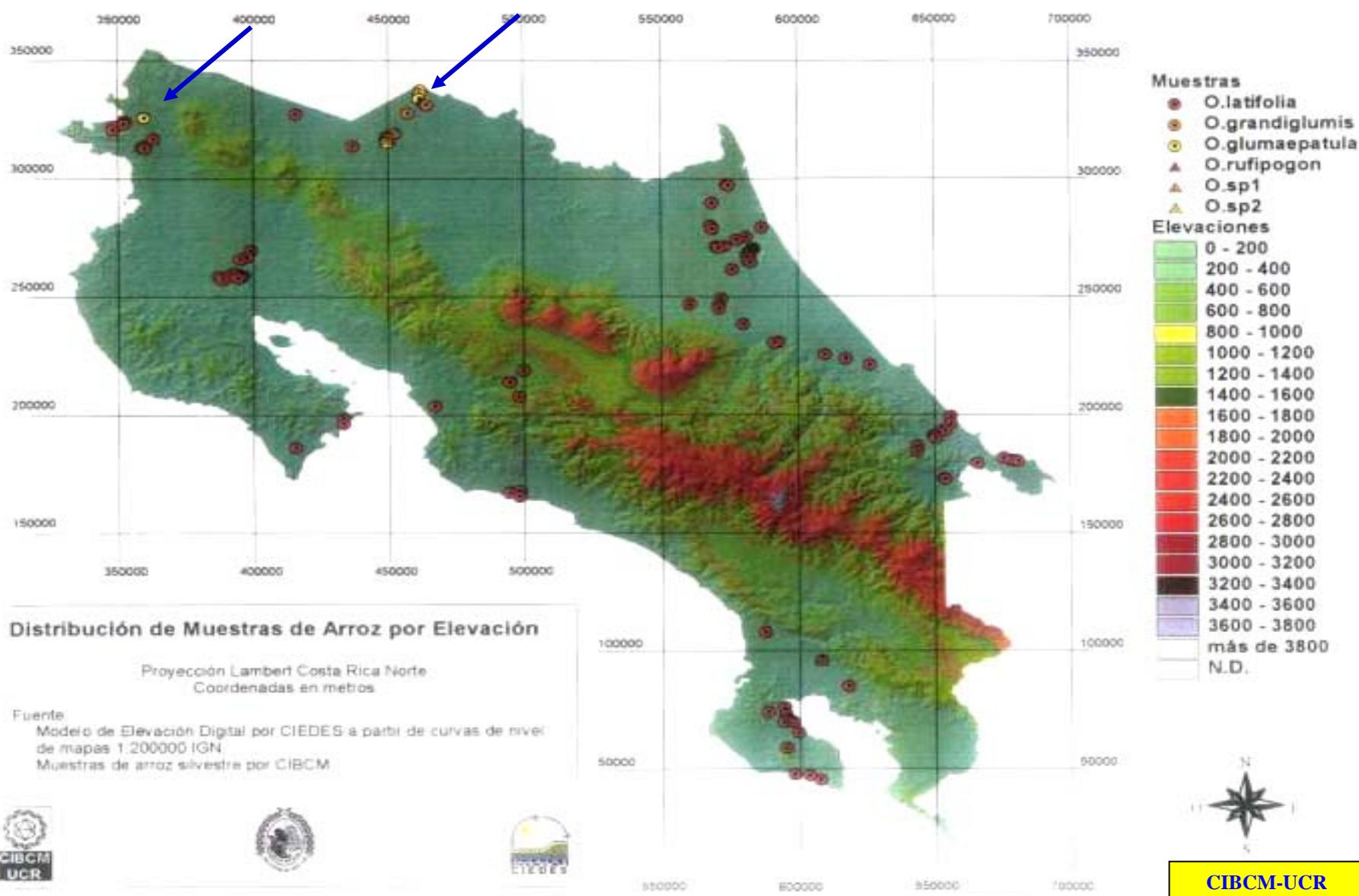
Oryza glumaepatula



Weedy rice



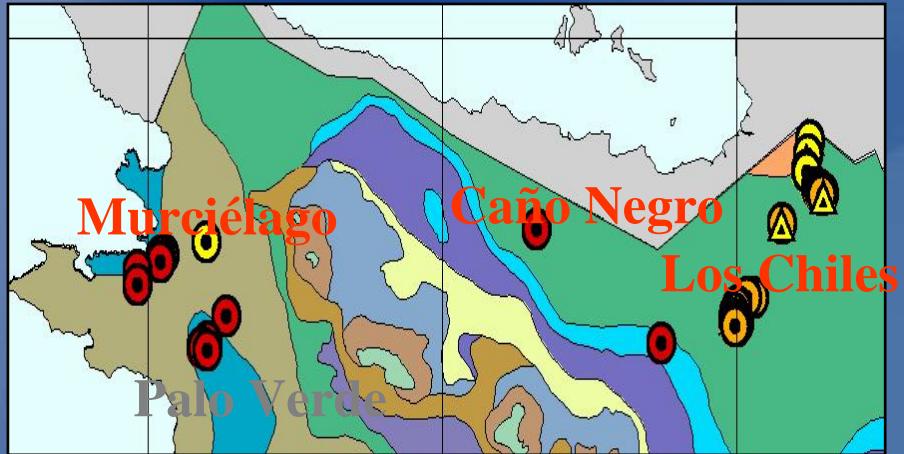
Distribution of wild *Oryza* populations in Costa Rica



Genome type of three native wild *Oryza* species of Costa Rica:

- *O. latifolia*: CCDD genome
 - *O. grandiglumis*: CCDD genome
 - *O. glumaepatula*: **AA** genome
-
- *O. sativa*: **AA** genome

Reproductive biology of *O. glumaepatula*



- The Medio Queso Wetland is home for millions of *O. glumaepatula* plants.
- Synchronize flowering in different localities.
 - Flowering period in November at the end of the rainy season.
- Rice commercial fields are grown in close proximity to *O. glumaepatula* (flowering period: August).

To study the reproductive biology of *O. glumaepatula* and its potential hybridization with *O. sativa*

To study the reproductive strategies of *O. glumaepatula*.

To determine the compatibility of *O. sativa* and *O. glumaepatula*.

To confirm the hybrid nature of the F₁ plants.

To determine seed set of the hybrids.

Methodologies

Reproductive biology

Selection of 19 progeny groups.



PCR

labelled-SSR



Genetic analyses with sequencer



Comparison of genetic profiles

Genetic compatibility

Flower emasculation



Hand made crosses
(O. glumaepatula
x *O. sativa*)



Seed set evaluation



Hybrid seed evaluation

In vitro germination of the F₁ seeds



Morphological analyses



PCR

labelled-SSR



Genetic analyses with sequencer

O. glumaepatula progeny studies using labelled-microsatellites

Typical
segregation of
self-pollinated
plants

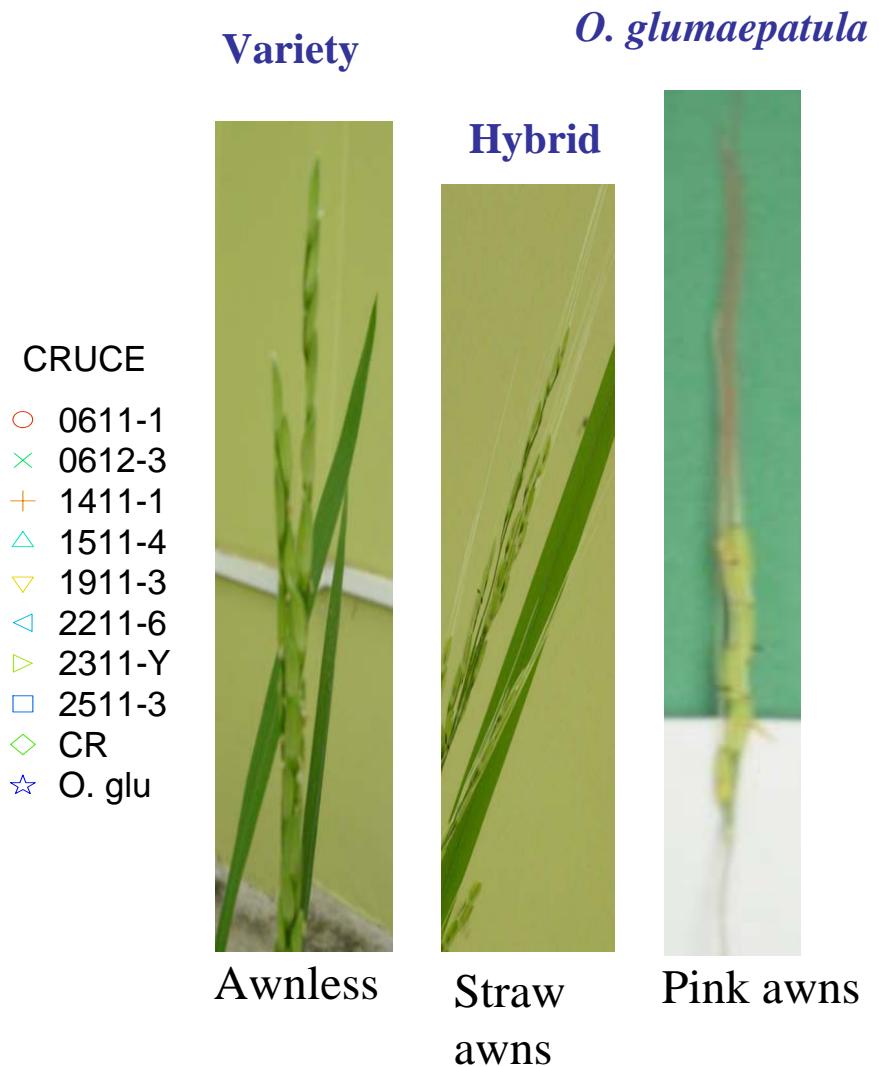
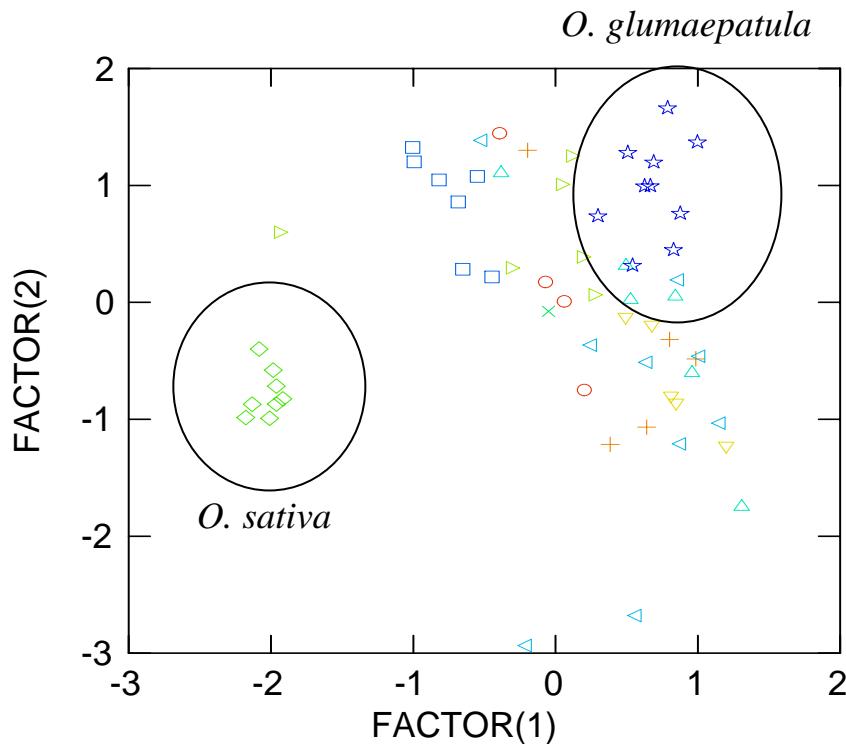
Sample	Family	RM5	RM13	RM17	RM22	RM255	RM38
I-1-2M	Female	ab	aa	aa	ab	aa	aa
I-1-2A	Progeny	ab	aa	aa	ab	aa	aa
I-1-2B	Progeny	bb	aa	aa	ab	aa	aa
I-1-2C	Progeny	ab	aa	aa	bb	aa	aa
I-1-2D	Progeny	ab	aa	aa	ab	aa	aa
I-1-2F	Progeny	aa	aa	aa	aa	aa	aa
I-1-2G	Progeny	ab	aa	aa	ab	aa	aa

Registration
of outcrossing
events

Family	RM5	RM13	RM17	RM22	RM255
Female	aa	aa	aa	aa	aa
Progeny	aa	aa	aa	aa	aa
Progeny	aa	aa	aa	aa	aa
Progeny	ab	aa	aa	aa	ab
Progeny	aa	aa	aa	aa	aa
Progeny	aa	aa	aa	aa	aa
Progeny	ab	aa	aa	aa	aa

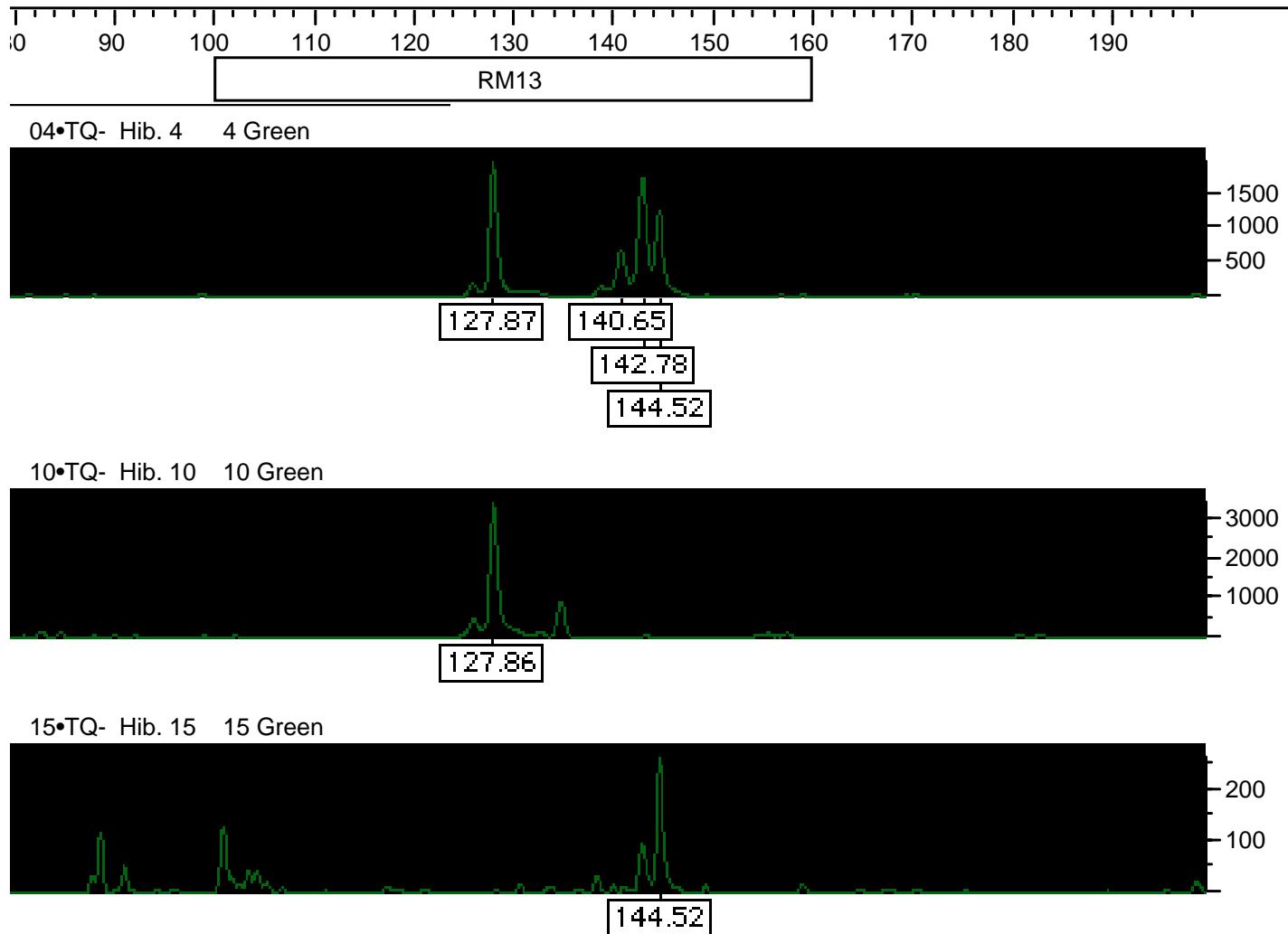
Evaluation of the hybrids using 12 morphological traits

Discriminant analysis



Factor 1	Factor 2
Plant size	Ligule length
Color of the culm base	Flag length
Color of the stigma	Awn color

Confirmation of the hybrid nature of the plants using fluorescent-labelled microsatellites

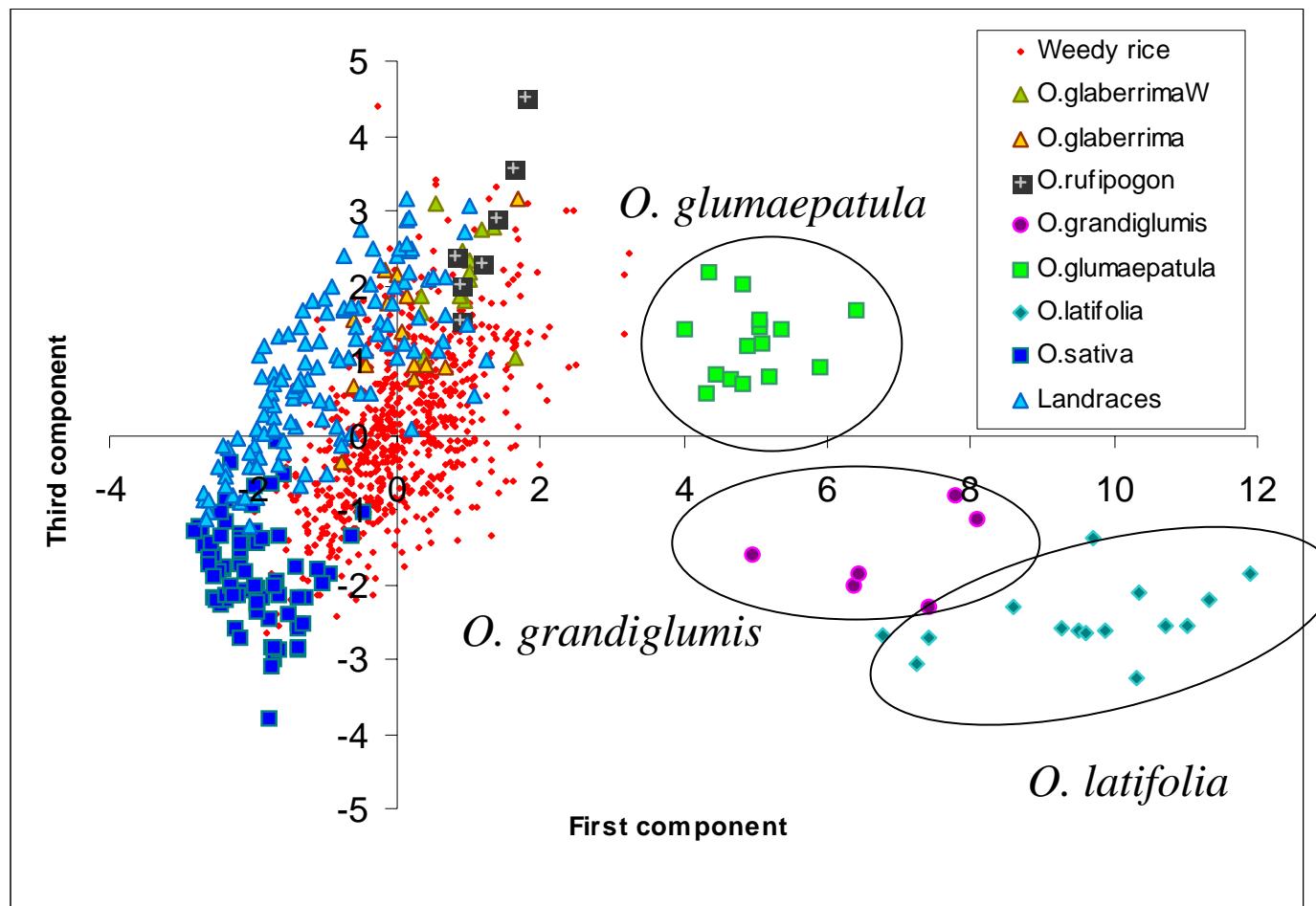


RM13 Genotyper Electropherogram

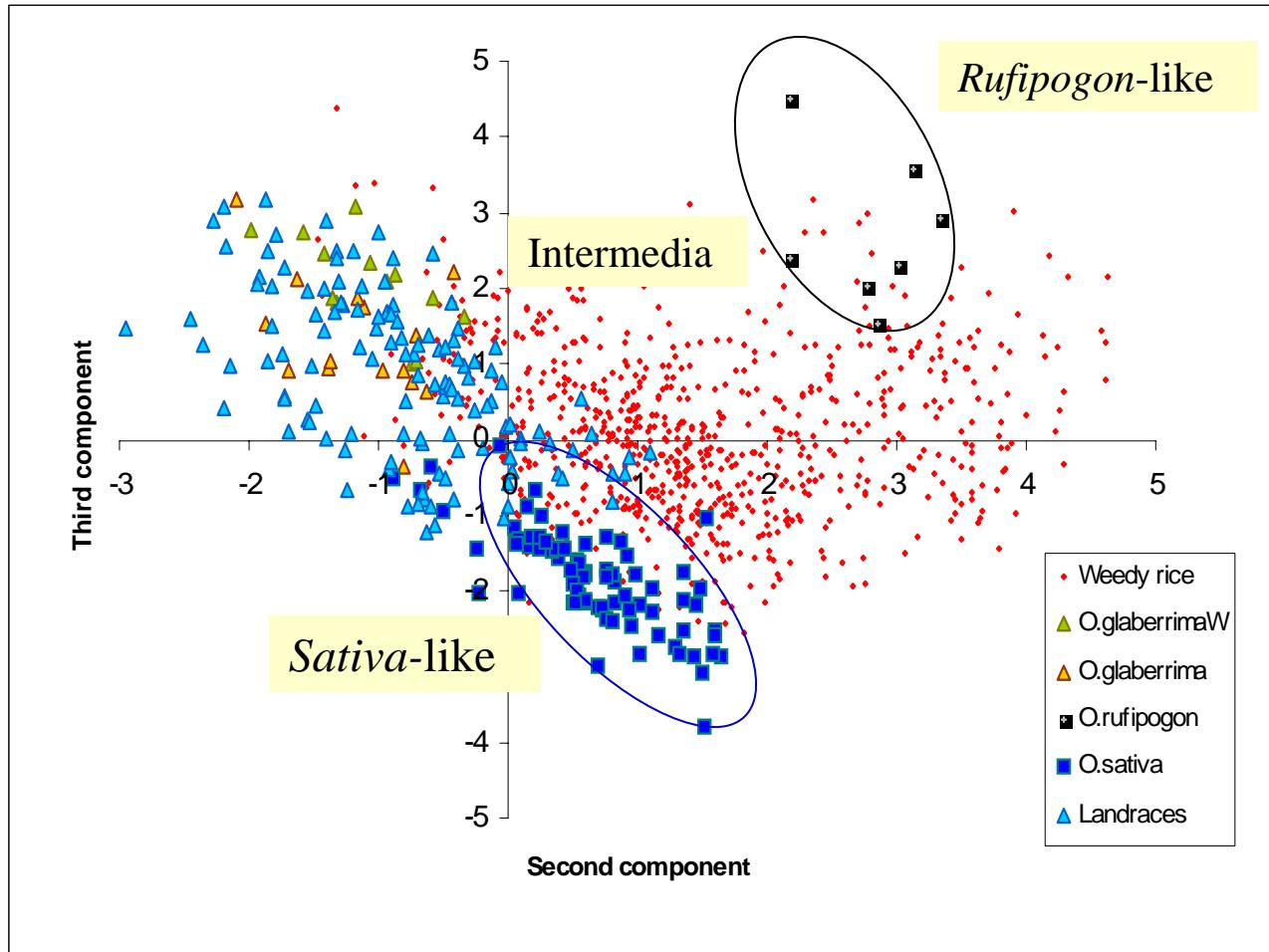
Conclusions

- *O. glumaepatula* is **autogamous** with few outcrossing events.
- Hybrids are **sterile**.
- Lack of flowering overlap between *O. glumaepatula* and *O. sativa*.
- The previous results suggest low probabilities of gene flow between these species. These information has important implications in terms of **biosafety**.

Morphologic characterization of Costa Rican weedy rice complex



Morphologic characterization of Costa Rican weedy rice complex



20
morphotypes
using seed
traits

3 main
groups:
sativa-like
intermedia
rufipogon-like

Evaluation of gene flow from transgenic rice variety to weedy rice

To assess gene flow from *O. sativa* to selected weedy rice morphotypes using two selection markers:

- The purple color of the culm of the variety Setesa-9.



- The resistance to ammonium glufosinate (PPT) of a transgenic rice line.



Evaluation of gene flow from Setesa-9 to weedy rice

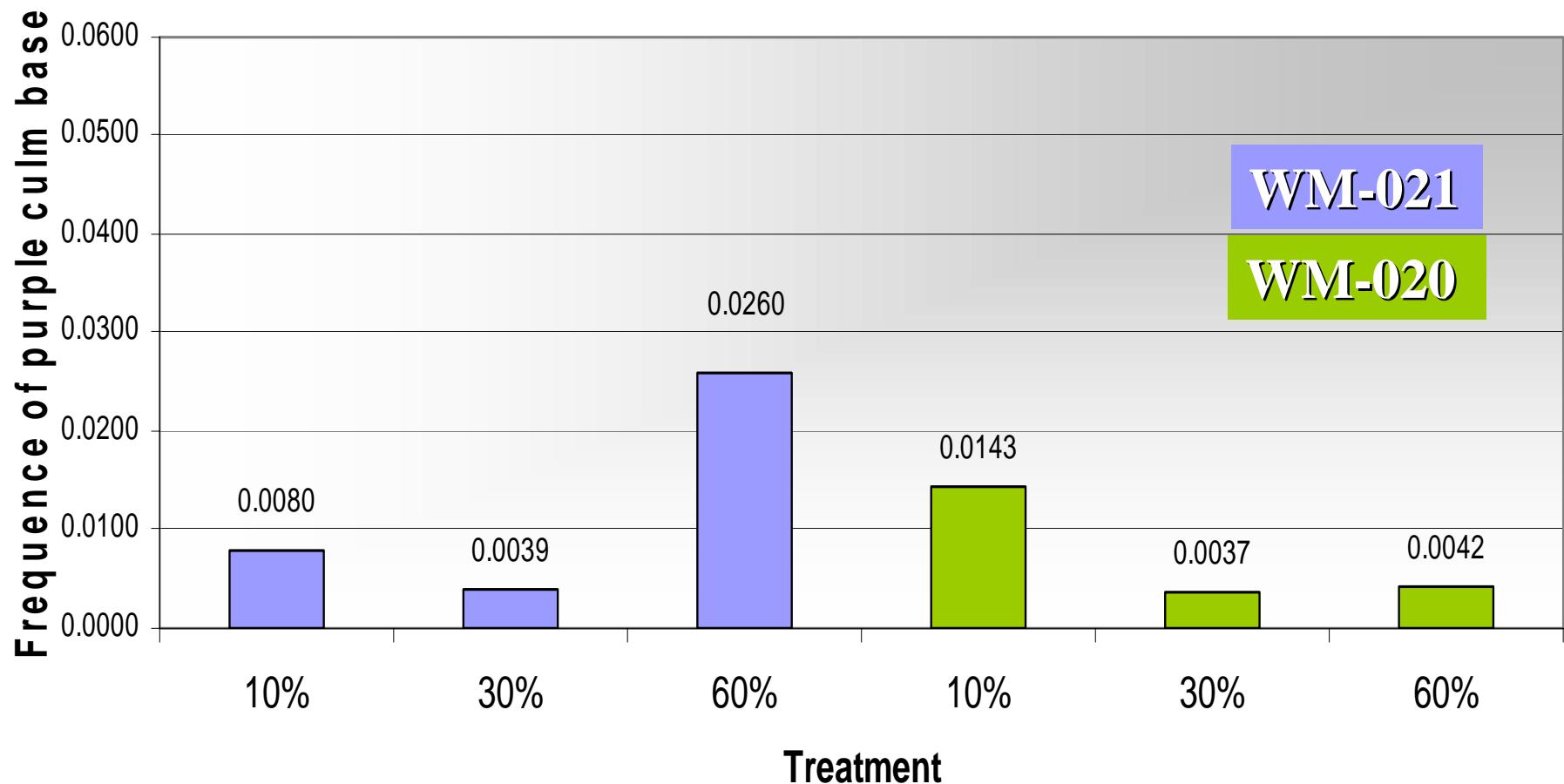
- Variety: **Setesa-9**
- Weedy rice morphotypes: **WM-020** and **WM-021**
- Plots of 2.25 m²
- Weedy rice infestation levels: **10%**, **30%** and **60%**
- Three replicates
- Seed harvest
- Evaluate F1(purple culm base)
- Confirmation of putative hybrids using SSR.



WM-020

Setesa –9

Frequency of putative hybrids Setesa 9 -weedy rice morphotypes



N = 55460

Evaluation of gene flow from transgenic rice line to weedy morphotypes

- Transgenic rice line
- Six weedy morphotypes.
- Plots with infestation levels:
10%, 15% and 30%
- 2 replicates 36 plots
- Harvest by rows 2 times/week
- PPT resistance in F₁.
- Hybrid confirmation by PCR.



Characteristics of weedy rice morphotypes used in the gene flow studies

	Weedy morphotype	Abundance in fields	Days to reach 50% antesis	Morphological classification
	WM-020	19.6%	118	Sativa-like
	WM-023	11.8%	101	Intermedia
	WM-073	2-5%	111	Intermedia
	WM-120	2-5%	115	Sativa-like
	WM-121	2-5%	106	Intermedia
	WM-329	7.1%	101	Rufipogon-like

Hybrid identification (preliminary results)

- 4200-8000 weedy rice seeds per plot + 800 control seeds.
- Seed emergence evaluated 15 days after seeding (DAS)
- Herbicide dose:
1st application 450g a.i./ha 30 DAS
2nd application 450g a.i./ha 40 DAS
- Evaluation 10 days after 2nd application



Results

- Weedy rice reproductive cycle



Morphotype	Classification	50% anthesis	Flowering overlap
WM-120	sativa-like	86	11
WM-020	sativa-like	90	14
WM-023	Intermedia	86	11
WM-121	Intermedia	86	14
WM-073	Intermedia	98	11
WM-329	rufipogon-like	90	7
AS10-7-14	transgenic line	98	

Frequency of weedy rice herbicide resistant plants

Morphotype	Infestation level	Number of resistant plants	Number of herbicide resistant plants		
			Plants evaluated	Frequency	Percentage
WM-020	10%	7	5350	0.00131	0.13
WM-020	15%	8	7410	0.00108	0.11
WM-020	30%	34	8105	0.00419	0.42
WM-023	10%	4	4293	0.00093	0.09
WM-023	15%	12	7438	0.00161	0.16
WM-023	30%	4	8000	0.00050	0.05
WM-073	10%	5	7282	0.00069	0.07
WM-073	15%	5	7826	0.00064	0.06
WM-073	30%	3	8321	0.00036	0.04
WM-120	10%	36	6844	0.00526	0.53
WM-120 (sl)	15%	54	7443	0.00726	0.73
WM-120	30%	58	8032	0.00722	0.72
WM-121	10%	6	7318	0.00082	0.08
WM-121	15%	3	5436	0.00055	0.06
WM-121	30%	13	9550	0.00136	0.14
WM-329	10%	8	5967	0.00134	0.13
WM-329	15%	7	7148	0.00098	0.1
WM-329 (rl)	30%	2	6815	0.00029	0.03
Total		269	128578	0.00209	0.21

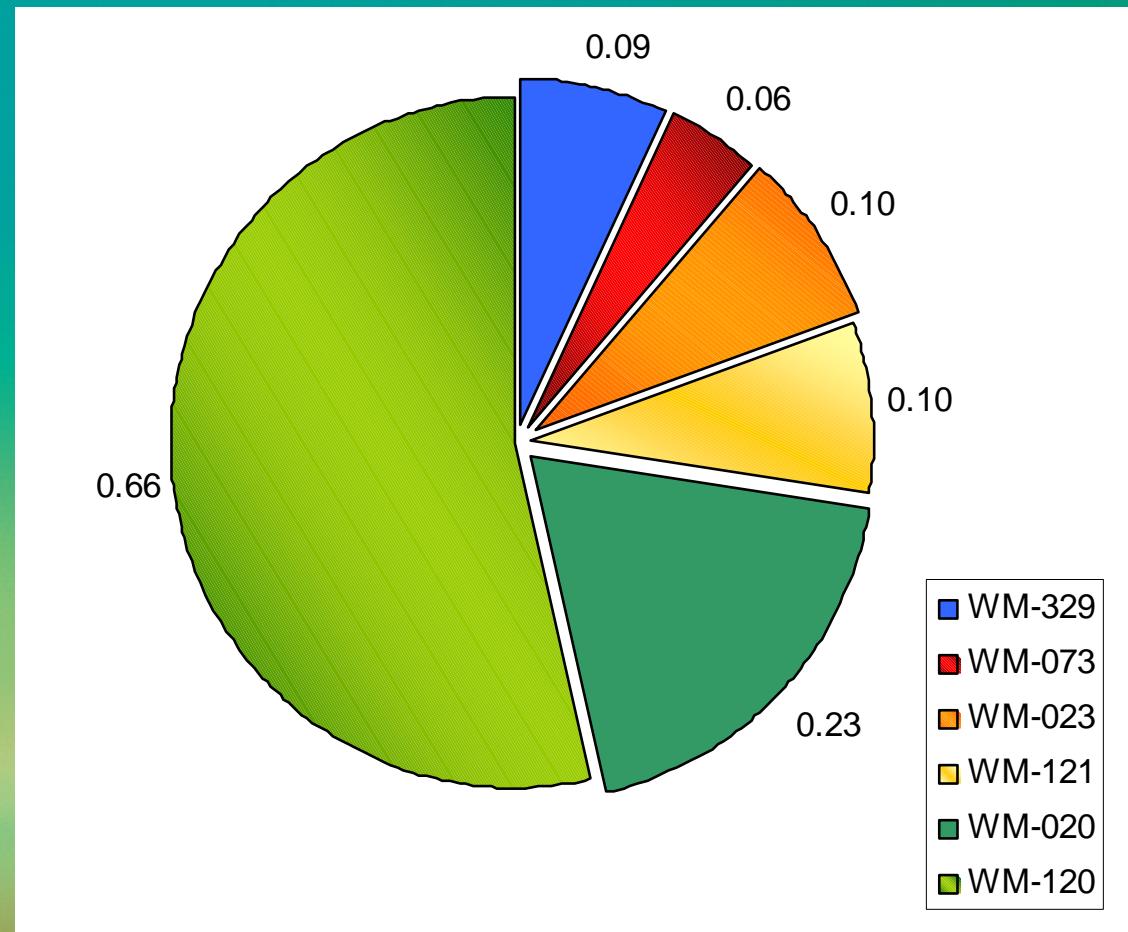


Hybrid bar⁺

Differences between morphotypes

Morphotype	Frequency
WM-120	0.0131 ^a
WM-020	0.0030 ^b
WM-023	0.0010 ^c
WM-121	0.0010 ^c
WM-329	0.0008 ^c
WM-073	0.0006 ^c

Medias comparison GLZ Proc
GENMOD SAS



Herbicide resistant plants per weedy rice morphotype

Conclusions

Gene flow weedy rice-Setosa-9

- Hybridization percentage were higher than those reported for *O. sativa*.
- The purple color could be inherited in a more complex way and have different degrees of penetrance.
- No differences were observed in hybrid frequency according to infestation levels.

Gene flow weedy rice-transgenic rice

- Hybridization between weedy rice and transgenic rice varied between 0.03% and 0.73%. Similar to other reports (Chen *et al.*, 2004; Messeguer *et al.*, 2004).
- Herbicide resistant plants were more common in sativa-like than in intermedia and rufipogon-like morphotypes.
- No differences were observed in hybrid frequency according to infestation levels.

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